suppressed patients as those with HIV infection, liver dysfunction, chronic pulmonary disease, malignancy, sarcoidosis, under corticosteroids or dialysis, transplant receivers and diabetics.
Objectives: We present the case of a 61-year old male with vasculitis associated necrotizing glomerulonephritis who developed disseminated cryptococcosis.
Methods: The patient was receiving corticosteroids, cyclophosphamide and mycophenolate mofetil for 3,5years due to necrotizing glomerulonephritis. He presented with Fournier's gangrene (fever, right orchiepididymitis and cellulitis of the lower extremities). Surgical exploration under broad-spectrum antibiotics was performed resulting in right orchiectomy. Histological examination revealed a glanulomatous necrotizing inflammation (Ziehl-Nielsen negative) and anti Tuberculous agents were added. He was intubated and transferred to ICU after developing oliguria, respiratory failure and shock. Erythematous lesions and ulcers appeared on his extremities. The daily dose of prednisolone was increased and antituberculous drugs were discontinued.
Results: Soon after admission on ICU, *cryptococcocus neoformans* was isolated in blood cultures. Brain CT scan and CSF were negative for cryptococcosis. Tissue biopsy from skin lesions showed acute panniculitis and fungi spores while culture isolated Cryptococcus neoformans. Further testis stains confirmed the presence of Cryptococcus. Amphotericin B (300mg/day) was added. His condition improved and he was extubated the 10th day. Six days later he became septic with respiratory failure and hemodynamic instability. Multiresistant Klebsiella pneumoniae was isolated in bronchial secretions and antibiotic therapy was modified. He developed refractory septic shock and multiorgan failure.
Conclusions: The presence of granulomas in a tissue biopsy should raise suspicion of autoimmune disorders, malignancy and systemic infections. Tuberculosis and fungal infections are suggested when there is history of immunosuppression. Skin lesions in cryptococcosis are a sign of dissemination. Secondary infections may complicate and worsen clinical course.

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Genome Analysis Reveals Horizontal Gene Transfer in *Penicillium marneffei*

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Background: *Penicillium marneffei* is the most important thermal dimorphic fungus causing respiratory, skin and systemic mycosis in Southeast Asia. The appearance of the HIV pandemic saw the emergence of the infection as an important opportunistic mycosis in immunocompromised patients. Besides HIV positive patients, *P. marneffei* infections have been reported in other immunocompromised patients. Despite its medical importance and its unusual thermal dimorphic capability, a large part of the ecology and epidemiology of *P. marneffei* remains unknown. The natural habitat of the fungus and its exact route of transmission have not been described. The advent of complete genome sequencing has led to the recognition of horizontal gene transfer (HGT) as a potentially important mechanism in the genome evolution in prokaryotes. In comparison, HGT is less well known in eukaryotes. As there are more and more eukaryotic whole genome sequencing become available, study of HGT among eukaryotic is possible.
Objectives: In this poster, we report the horizontal transfer of several genes from bacterial lineages that known to populate the soil environment. These events might be clues to the natural habitat of *P. marneffei* and provide insight on its ecology in the natural environment.
Methods: *P. marneffei* strain PM1 wan isolated from a HIV-negative patient with culture-documented penicilliosis in Hong Kong. The genome was sequenced and assembled. Potentially horizontally transferred genes are identified by BLAST against NCBI GenBank database. Sequences of selected *P. marneffei* genes were manually corrected. *P. marneffei* strain PM1 was cultured and the target genes were sequenced.
Results: A total of 10,060 genes were predicted in the *P.marneffei* genome by FGENESH. 9927 informative genes were subjected to BLAST search, 288 of them were found to have a better alignment with the bacterial sequences that the reference *A. fumigatus*, *A.nudulans* and *N. crassa* sequences. 6 genes were identified to be HGT candidates with good support from the trees constructed by phylogenetic methods. Phylogenies of HGT candidates are suggestive of transfer mainly from soil bacteria, especially proteobacteria.
Conclusion: We were able to identify reliably 6 genes from *P. marneffei* that are potential HGT candidates. And the soil-derived bacteria source of these 6 genes provided evidence for *P. marneffei* to be a soil organism.

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Drug-resistant *Mycobacterium tuberculosis* in Argentinian Children

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Background: The emergence of strains of *Mycobacterium tuberculosis* (TB) that are resistant to antimycobacterial agents (Drug-resistant or DR-TB) is a worldwide problem, whose magnitude is not well described especially in pediatric patients. TB sensibility surveillance and risk factors for DR-TB are important issues to consider at the start of treatment.
Objective: To identify the clinical features, risk factors, and outcome of pediatric patients with DR- TB.
Methods: We performed a retrospective review of medical records of 19 pediatric patients, with culture confirmed DR-TB, between January 1998 to December 2007 at the Garrahan Pediatric Hospital. Drug resistance tests to first line drugs (INH, RMP, SM, EMB) were performed on Lowenstein- Jensen medium according to the proportion method or/and Bactec 460 TB system. We defined DR-TB to those strains of *M. tuberculosis* resistant to one or more first line drugs. Depending on the number of drugs, we divided in single or resistant to 2 or more drugs. In the last group, we recorded the data in two mutually exclusive categories: multidrug resistant TB strains (MDR-TB, those resistant at least to INH+RMP), and resistant to 2 or more drugs (those resistant to any combination other than INH+RMP)
Results: We had 797 TB cases during 9 years; 299 patients had bacteriologically confirmed positive culture (37%). Nineteen strains (6.3%) were DR-TB. Primary resistance was found in 15/19 patients (80%).The median age of the patients was 84 months (r: 7-168), 9 patients were immunocompromised (8 of them HIV positive). Pulmonary disease was the most common presentation: 15 patients (79%). From 19 DR-TB cultures 11 (58%) were mono-resistant (80% to INH), and 8 (42%) resistant to 2 or more drugs. Six of them (75%) were MDR-TB. DR- TB infection was more frequent in immunocompromised patients 9/19, especially for those that are MDR-TB: 8 patients (89%). Nine (48%) had TB contact, 7 patients (37%) had previous hospital admission, and 4 patients (21%) previous TB treatment. Two patients (10%) died because of TB, of central nervous system infection.
Conclusion: DR-TB is infrequent in pediatric patients. The immunocompromised state is an important risk factor associated with resistance in this population.